

Amendments to the Specification

Please delete the text starting at page 17, line 21 to page 19, line 7:

~~Provided below is the sequence listing information for SEQ ID Nos. 1, 2 and 3~~

SEQUENCE LISTING

GENERAL INFORMATION

~~APPLICANT: CSIR~~

~~TITLE OF INVENTION: Method for the detection of predisposition to high altitude pulmonary edema (HAPE).~~

~~NUMBER OF SEQUENCES: 03~~

~~CORRESPONDING ADDRESS: Institute of genomics and integrative biology, CSIR, Delhi University Campus, Mall Road-110007, India.~~

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INFORMATION FOR SEQUENCE ID NO: 1

1. SEQUENCE CHARACTERISTICS

~~1. LENGTH: 258 bp~~

~~2. TYPE: DNA~~

~~5'CAG CGG AGT GAT GGC AAG CAC GAC TTC CGG GTG TGG AAT GCT CAG
CTC ATC CGC TAT GCT GGC TAC CAG ATG CCA GAT GGC AGC ATC AGA GGG
GAC CCT GCC AAC GTG GAA TTC ACT CAG GTA CCC GGC CCA GCC TCA GCC
A*/GCC GGC CAT TGG GGC GGG GAG CCC CGT GGT GAG CGA GTG ACA GAG
TGG AGC CCA GAG GAG ACA CGC AGC CCG GGC TTA CAG ACT CAC AGG GCC
CGT CTT GTT CCC CAG CTG TGC ATC 3'~~

~~3. ORGANISM: *Homo sapiens* (Humans)~~

~~4. IMMEDIATE SOURCE: PCR~~

~~5. NAME/KEY: Marker Region~~

~~6. SEQUENCE ID #1~~

INFORMATION FOR SEQUENCE ID NO: 2

~~1. SEQUENCE CHARACTERISTICS~~

~~LENGTH: 24 bp~~

~~TYPE: DNA~~

~~5' CAG CGG AGT GAT GGC AAG CAC GAC 3'~~

~~ORGANISM: Artificial sequence~~

~~IMMEDIATE SOURCE: Synthetic~~

~~NAME/KEY: Synthetic Oligonucleotide~~

~~SEQUENCE ID #2~~

INFORMATION FOR SEQUENCE ID NO: 3

~~1. SEQUENCE CHARACTERISTICS~~

~~LENGTH: 24 bp~~

~~TYPE: DNA~~

~~5' GAT GCA CAG CTG GGG AAC AAG ACG 3'~~

~~ORGANISM: Artificial sequence~~

~~IMMEDIATE SOURCE: Synthetic~~

~~NAME/KEY: Synthetic Oligonucleotide~~

~~SEQUENCE ID #3~~

Amendments to the Drawings:

The attached sheet of drawings includes a change to the text of Figure 1. The text of the figure legend of Figure 1 has been deleted and the attached amended Figure 1 is labeled "Replacement Sheet" at the top of the page.

The text of the figure legend which was deleted stated "Schematic representation of the gene of inducible Nitric Oxide Synthase (iNOS) localization: 17 cenq^{11.2}. The vertical bars showing the exonic regions (From Gene bank Nucelotide Sequence ID No. NT-_010799)."